

L8.1

### Lectures

## Thiol reduction systems: linking stress signalling to plant development

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The redox homeostasis is a critical parameter controlling plant development in response to biotic and abiotic stress. NADPH-Thioredoxin System (NTS) and NADPH-Glutathione/Glutaredoxin System (NGS) are key pathways regulating the redox homeostasis. In order to decipher the functions of and the interplays between these redox pathways, we performed a genetic approach in *Arabidopsis thaliana*. This talk will give an overview of the outcome of this approach. Major data show that alternative reduction pathways are acting between NGS and NTS and that thiol reduction pathways are playing key roles in plant development in response to environmental constraints, notably influencing pollen fertility, meristematic activities and hormone signalling.

L8.2

# Ca<sup>2+</sup> waves and ROS in long distance root-to-shoot signalling

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The sessile plant lifestyle requires being highly sensitive to multiple environmental signals and integrating them to regulate developmental and physiological responses. Such stimuli are often highly localized but can lead to changes ranging from activation of biochemical signalling networks to changes in gene expression throughout the plant. The relatively slow redistribution of regulators such as peptides, RNAs, ions, metabolites and hormones has been shown to mediate some of this systemic signalling response. However, rapid communication within the plant also exists and has been proposed to involve signals ranging from action and system potentials to reactive oxygen species. We have identified a further element of this rapid signalling system in  $Ca^{2+}$  waves that propagate through the plant at rates of up to 400 µm/sec. In the case of local salt stress to the root, these  $Ca^{2+}$  waves propagate through the cortex and endodermal cell layers.  $Ca^{2+}$  wave generation requires the vacuolar ion channel TPC1 and is partially dependent on ROS produced from AtRBOHD. This  $Ca^{2+}$  wave system appears required to elicit systemic molecular responses in target organs and to contribute to whole plant stress tolerance.

08.1

#### **Oral presentations**

## Transport of glutathione between the cytosol and the nucleus: investigation of candidate proteins in *Arabidopsis thaliana*

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In plant and animal cells, the tripeptide thiol glutathione (GSH) accumulates in the nucleus early in the cell cycle. GSH depletion leads to an arrest of the cell cycle at G1 phase and impairs the formation of a functional root meristem in plants. The B-cell lymphoma 2 (Bcl-2) protein is required for the import of GSH into mitochondria and nuclei of mammalian cells. Whereas no Bcl-2 homologues have been identified in plants, homologues of the Bcl-2 associated athanogene (BAG) proteins are found in plant genomes. There are 7 BAG genes in *Arabidopsis thaliana* and at least 3 of these have been shown to function in stress resistance and the regulation of cell death. In addition, deficiency of the WD-repeat protein ALADIN, which is a component of the nuclear pore complex (NPC), causes an arrest of the cell cycle at G1 in proliferating human cells. We therefore investigated the role of the BAG and ALADIN-related proteins in *Arabidopsis* by characterising the growth and development of knockout lines. Our overall aim was to test the hypothesis that these proteins are involved in the transport of GSH into the nucleus during the cell cycle. Data on the growth phenotypes and redox status of the knockout mutants will be presented.

08.2

## Redox-mediated regulation of wheat seed dormancy revealed through modification-specific proteomics

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Physiological seed dormancy is under the control of two distinct processes, the accumulation of damaging ROS and RNS, and a hormonal balance which regulates dormancy directly and also interacts with ROS and antioxidative pathways. The role of redox active proteins that undergo reversible cysteine oxidation in dormant, non-dormant, ABA and GA treated seed protein extracts from a wheat cultivar with extreme dormancy was addressed by a thiol-redox proteomic approach. The total and redox-sensitive proteomes were quantitatively monitored by 2D-gel mapping, fluorescent thiol-specific labelling, and mass spectrometry analysis in conjunction with wheat EST sequence libraries. Comparative analysis of hybrid lines of spring wheat (*Triticum aestivum* L.) was used to gain further insight into mechanisms of dormancy control. The results give an insight into the dormancy-related alteration of thiol-redox profiles in seed proteins that function in a number of major processes in seed physiology, and provide evidence for a shift in the accumulation of proteins from those active in biosynthesis and metabolism to those with roles in storage and protection against biotic and abiotic stresses in wheat seeds of high dormancy genotypes.